>lcl|3831 unnamed protein product
Length=506

 Score = 979 bits (2531), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 477/515 (92%), Positives = 485/515 (94%), Gaps = 19/515 (3%)

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Query  1    MTSINVKLLYHYVITNLFNLCFFPLTAIVAGKASRLTIDDLHHLYYSYLQHNVITIAPLF  60
            MTSINVKLLYHYVITNLFNLCFFPLTAIVAGKA RLTIDDLHHLYYSYLQHN+ITIAPLF
Sbjct  1    MTSINVKLLYHYVITNLFNLCFFPLTAIVAGKAYRLTIDDLHHLYYSYLQHNLITIAPLF  60

Query  61   AFTVFGSILYIVTRPKPVYLVEYSCYLPPTQCRSSISKVMDIFYQVRKADPFRNGTCDDS  120
            AFTVFGS+LYI TRPKPVYLVEYSCYLPPT CRSSISKVMDIFYQVRKADP RNGTCDDS
Sbjct  61   AFTVFGSVLYIATRPKPVYLVEYSCYLPPTHCRSSISKVMDIFYQVRKADPSRNGTCDDS  120

Query  121  SWLDFLRKIQERSGLGDETHGPEGLLQVPPRKTFAAAREETEQVIVGALKNLFENTKVNP  180
            SWLDFLRKIQERSGLGDETHGPEGLLQVPPRKTFAAAREETEQVI+GAL+NLF+NT VNP
Sbjct  121  SWLDFLRKIQERSGLGDETHGPEGLLQVPPRKTFAAAREETEQVIIGALENLFKNTNVNP  180

Query  181  KDIGILVVNSSMFNPTPSLSAMVVNTFKLRSNVRSFNLGGMGCSAGVIAIDLAKDLLHVH  240
            KDIGILVVNSSMFNPTPSLSAMVVNTFKLRSNVRSFNLGGMGCSAGVIAIDLAKDLLHVH
Sbjct  181  KDIGILVVNSSMFNPTPSLSAMVVNTFKLRSNVRSFNLGGMGCSAGVIAIDLAKDLLHVH  240

Query  241  KNTYALVVSTENITYNIYAGDNRSMMVSNCLFRVGGAAILLSNKPRDRRRSKYELVHTVR  300
            KNTYALVVSTENITYNIYAGDNRSMMVSNCLFRVGGAAILLSNKP DRRRSKYELVHTVR
Sbjct  241  KNTYALVVSTENITYNIYAGDNRSMMVSNCLFRVGGAAILLSNKPGDRRRSKYELVHTVR  300

Query  301  THTGADDKSFRCVQQGDDENGKTGVSLSKDITEVAGRTVKKNIATLGPLILPLSEKLLFF  360
            THTGADDKSFRCVQQGDDENGK GVSLSKDIT+VAGRTVKKNIATLGPLILPLSEKLLFF
Sbjct  301  THTGADDKSFRCVQQGDDENGKIGVSLSKDITDVAGRTVKKNIATLGPLILPLSEKLLFF  360

Query  361  VTFMAKKLFKDKVKHYYVP-----IDHFCIHAGGR-----LEKNLGLAPIDFKLAAVIDV  410
            VTFM KKLFKDK+KHYYVP     IDHFCIHAGGR     LEKNL LAPID
Sbjct  361  VTFMGKKLFKDKIKHYYVPDFKLAIDHFCIHAGGRAVIDVLEKNLALAPID--------  411

Query  411  VEASRSTLHRFGNTSSSSIWYELAYIEAKGRMKKGNKVWQIALGSGFKCNSAVWVALSNV  470
            VEASRSTLHRFGNTSSSSIWYELAYIEAKGRMKKGNKVWQIALGSGFKCNSAVWVAL+NV
Sbjct  412  VEASRSTLHRFGNTSSSSIWYELAYIEAKGRMKKGNKVWQIALGSGFKCNSAVWVALNNV  471

Query  471  KASTNSPWEHCIDRYPVKIDSDSAKSETRAQNGRS  505
            KASTNSPWEHCIDRYPVKIDSDS KSETR QNGRS
Sbjct  472  KASTNSPWEHCIDRYPVKIDSDSGKSETRVQNGRS  506
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